

Tue May 1 15:15:31 2001

us-09-142-970-1.ra1

Page 1

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

Seq 1

OM protein - protein search, using sw model

Run on: May 1, 2001, 14:48:53 ; Search time 37.5 Seconds
(without alignments)
53.278 Million cell updates/sec

Title: US-09-142-970-1

Perfect score: 558
Sequence: 1 LYKKNRYALSKSGSVNAPNRFLLTGTLNGKISVTG 104

Scoring table:
BIOSUM62
Gapop 10.0 , Gapext 0.5

Shed: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Issued Patents, AA:*

- 1: /cgcn2_6/prodata/2/1aa/5A.COMB.pep:*
- 2: /cgcn2_6/prodata/2/1aa/5B.COMB.pep:*
- 3: /cgcn2_6/prodata/2/1aa/6A.COMB.pep:*
- 4: /cgcn2_6/prodata/2/1aa/6B.COMB.pep:*
- 5: /cgcn2_6/prodata/2/1aa/6C.COMB.pep:*
- 6: /cgcn2_6/prodata/2/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	485	86.9	1507	6	Patent No. 5268270-2
2	329.5	59.1	1541	5	PCT-US95-10661A-3
3	322.5	57.8	1702	5	PCT-US95-10661A-5
4	320.5	57.4	1545	5	PCT-US95-10661A-6
5	311.5	55.8	1848	5	PCT-US95-10661A-4
6	114	20.4	1394	5	PCT-US95-10661A-2
7	75	13.4	1577	2	Sequence 2, Appli
8	73.5	13.2	631	1	US-08-487-890A-115
9	73.5	13.2	631	2	US-08-478-435-115
10	73.5	13.2	631	2	US-08-337-483-115
11	73.5	13.2	631	2	US-08-478-373-115
12	73.5	13.2	631	3	US-08-474-671-115
13	73.5	13.2	631	3	US-08-483-577A-115
14	72	12.9	430	2	US-08-945-848-8
15	71	12.7	806	1	US-07-980-528-2
16	67.5	12.1	631	1	US-08-487-890A-111
17	67.5	12.1	631	2	US-08-478-435-111
18	67.5	12.1	631	2	US-08-337-483-111
19	67.5	12.1	631	2	US-08-478-373-111
20	67.5	12.1	631	3	US-08-474-671-111
21	67.5	12.1	631	3	US-08-483-577A-111
22	67.5	12.1	890	2	US-08-483-101-14
23	66	11.8	434	2	US-08-795-475-3
24	66	11.8	648	1	US-08-487-890A-109
25	66	11.8	648	2	US-08-478-435-109
26	66	11.8	648	2	US-08-337-483-109
27	66	11.8	648	2	US-08-478-373-109

28	66	11.8	648	3	US-08-474-671-109	Sequence 109, App
29	66	11.8	648	3	US-08-483-577A-109	Sequence 109, App
30	64.5	11.6	275	2	US-08-900-565-4	Sequence 4, Appli
31	64.5	11.6	453	6	5510466-4	Patent No. 5510466
32	64.5	11.6	1618	1	US-07-853-913-4	Sequence 4, Appli
33	64	11.5	394	3	US-08-673-814-6	Sequence 6, Appli
34	64	11.5	1338	2	US-08-728-470-9	Sequence 9, Appli
35	64	11.5	1599	2	US-08-617-697-9	Sequence 22, Appli
36	63	11.3	708	3	US-08-613-009A-22	Sequence 10, Appli
37	63	11.3	1529	2	US-08-728-470-10	Sequence 10, Appli
38	63	11.3	1600	2	US-08-617-697-10	Sequence 13, Appli
39	62.5	11.2	671	2	US-08-737-716-13	Sequence 1, Appli
40	62	11.1	305	2	US-08-795-475-1	Sequence 113, App
41	62	11.1	630	1	US-08-487-890A-113	Sequence 113, App
42	62	11.1	630	2	US-08-478-435-113	Sequence 113, App
43	62	11.1	630	2	US-08-337-483-113	Sequence 113, App
44	62	11.1	630	2	US-08-478-373-113	Sequence 113, App
45	62	11.1	630	3	US-08-474-671-113	Sequence 113, App

ALIGNMENTS

RESULT 1
5268270-2
Patent No. 5268270
APPLICANT: Meyer, Thomas F.; Halter, Roman; Pohlnier, Johannes
TITLE OF INVENTION: PROCESS FOR PRODUCING PROTEINS USING GRAM
NEGATIVE HOST CELLS
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/171,872
FILING DATE: 01-JUL-1987
SEQ ID NO: 2
LENGTH: 1507
5268270-2

Query Match 86.9%; Score 485; DB 6; Length 1507;
Best Local Similarity 86.5%; Pred. No. 4.8e-50;
Matches 90; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 LYKKNRYALSKSGSVNAPMPENGOTENNMDILMSTOEAKKAMNKKNRISGFSG 60
DB 559 LYKKNRYALSKSGSVNAPMPENGVAENNDIMPYGTGEAKKAMNKKNRIRIGDESG 618
QY 61 FGEENGKGNALNLFNGKSAONRFLTLTGTLNGKISVTG 104
DB 619 FDEENGKGNALNLFNGKSAONRFLTLTGTLNGKISVTG 662
RESULT 2
PCT-US95-10661A-3
Sequence 3, Application PC/TUS9510661A
GENERAL INFORMATION:
APPLICANT: Washington University, et al.
TITLE OF INVENTION: Haemophilus Adherence and Penetration Protein
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Honbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10661A
FILING DATE: 16-AUG-1995

OM protein - protein search, using sw model

Run on: May 1, 2001, 14:50:33 ; Search time 43.98 Seconds
(without alignments)
162.510 Million cell updates/sec

Title: US-09-142-970-1

Perfect score: 558
Sequence: 1 LYKKNRYRYALKSGSYNAP.....NRFLLTGNTLNKISVTGG 104

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.67:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558	100.0	1561	2 S61314	IgA-specific metal
2	558	100.0	1773	2 A81937	IgA-specific metal
3	554	99.3	1815	2 C81169	IgA-specific metal
4	488	87.5	1532	2 A26039	IgA-specific metal
5	329.5	59.1	1541	2 A37023	IgA-specific metal
6	328.5	58.9	1684	2 H64106	IgA-specific metal
7	328.5	58.9	1702	2 A41859	IgA-specific metal
8	320.5	57.4	1545	2 B41859	IgA-specific metal
9	317.5	56.9	1849	2 C41859	IgA-specific metal
10	128	22.9	1431	2 A81018	serine-type peptid
11	115.5	20.7	709	2 C64057	IgA-specific metal
12	115	20.6	1449	2 B81963	IgA-specific serin
13	114	20.4	1394	2 S60762	IgA-specific serin
14	111	19.9	1457	2 D81019	adhesion and penet
15	84.5	15.1	243	2 T24981	hypothetical prote
16	82.5	14.8	451	2 A23535	clustered asparagi
17	80.5	14.4	642	2 B75330	probable flagellar
18	80	14.3	629	2 B75330	probable ribosomal
19	79	14.2	2529	2 B64635	toxin-like outer m
20	78	14.0	568	2 JC7210	molluscan shell m
21	78	14.0	2399	2 H71879	toxin-like outer m
22	77.5	13.7	419	2 T40014	probable vesicular
23	76.5	13.7	1650	2 T18444	hypothetical prote
24	76	13.6	321	2 B37050	hypothetical glyci
25	75.5	13.5	484	2 G70846	endo-1,4-beta-xyla
26	75.5	13.5	954	2 S20907	hypothetical prote
27	75	13.4	697	2 T16306	glucosyltransferas
28	75	13.4	1577	2 T30858	glucosyltransferas
29	74.5	13.4	719	2 S61046	ARPI protein - yea

30	74.5	13.4	1596	2 A33106	neurogenic locus m
31	73.5	13.2	631	2 S70910	transferrin-bindin
32	73	13.1	1449	2 T30857	glucosyltransferas
33	72.5	13.0	125	2 T24982	hypothetical prote
34	72.5	13.0	234	2 S14469	asparagine-rich pr
35	72	12.9	402	2 T13614	N-acetyltransferas
36	72	12.9	712	2 E81196	transferrin-bindin
37	72	12.9	1367	2 T18466	hypothetical prote
38	72	12.9	1556	2 S76781	glutamate synthase
39	71.5	12.8	515	2 S20493	endoglucanase - C1
40	71.5	12.8	698	2 JH0163	No-on-transient A
41	71.5	12.8	700	2 JH0162	hypothetical prote
42	71.5	12.8	764	2 H71607	hypothetical prote
43	71	12.7	163	2 T23076	arabinogalactan-pr
44	71	12.7	461	2 T10265	asparagine-rich pr
45	71	12.7	537	2 A23770	

ALIGNMENTS

RESULT 1
S61314
IgA-specific metalloendopeptidase (EC 3.4.24.13) homolog - Neisseria meningitidis
C:Species: Neisseria meningitidis
A:Variety: HF13
C:Date: 20-Jul-1996 #sequence-revision 13-Mar-1997 #text-change 08-Dec-2000
C:Accession: S61314
R.Lombolt, H.; Poulsen, K.; Mogens, K.
Mol. Microbiol. 15, 495-506, 1995
A:Title: Comparative characterization of the iga gene encoding IgA1 protease in Neiss
A:Reference number: S61314; MUID:95302961
A:Accession: S61314
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1561 <LDM>
A:Cross-References: EMBL:X82474; NID:g732873; PIDN:CA57857.1; PID:g732874
A:Superfamily: IgA-specific metalloendopeptidase
C:Keywords: hydrolase; metalloproteinase

Query Match 100.0%; Score 558; DB 2; Length 1561;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYKKNRYRYALKSGSYNAPMPENGOTENNNDWILMGSTOEAKKNNKNNRISGFSG 60
|||||
DB 584 LYKKNRYRYALKSGSYNAPMPENGOTENNNDWILMGSTOEAKKNNKNNRISGFSG 643
QY 61 FFEENCKGHGALNLFNCKSAONRFLTGNTLNKISVTGG 104
|||||
DB 644 FFEENCKGHGALNLFNCKSAONRFLTGNTLNKISVTGG 687

RESULT 2
A81937
IgA-specific metalloendopeptidase (EC 3.4.24.13) NMA0905 [Imported] - Neisseria menin
C:Species: Neisseria meningitidis
A:Variety: group A strain Z2491, strain HF117, strain HF159, strain SM1027
C:Date: 05-May-2000 #sequence-revision 05-May-2000 #text-change 08-Dec-2000
C:Accession: A81937; S61317; S61318; S61321
R.Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mc
Holroyd, S.; Jørgensen, K.; Leather, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
A:Reference number: A81775; MUID:20222536
A:Accession: A81937
A:Molecule type: DNA
A:Residues: 1-1773 <PAR>
A:Cross-References: GB:AL157954; GB:AL157959; NID:g7379424; PIDN:CAB84182.1; PID:g737
A:Experimental source: serogroup A, strain Z2491
R.Lombolt, H.; Poulsen, K.; Mogens, K.

MOL. Microbiol. 15, 495-506, 1995
A:Title: Comparative characterization of the iga gene encoding Iga1 protease in *Neisseria*
A:Reference number: S61314; MUID:95302961
A:Accession: S61317
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 53-548 <LOW>
A:Cross-references: EMBL:X82470; NID:9732854; PIDN:CAA57853.1; PID:9732855
A:Experimental source: strain HF117
A:Accession: S61318
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 53-548 <LOW>
A:Cross-references: EMBL:X82471; NID:9732858; PIDN:CAA57854.1; PID:9732859
A:Experimental source: strain HF159
A:Accession: S61321
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 53-548 <LOW>
A:Cross-references: EMBL:X82472; NID:9732852; PIDN:CAA57855.1; PID:9732853
A:Experimental source: strain SM1027
C:Genetics:
A:Gene: iga; NMA0905
C:Family: Iga-specific metalloendopeptidase
C:Enzyme: hydrolase; metalloproteinase

Query Match 100.0%; Score 558; DB 2; Length 1773;
Best Local Similarity 100.0%; Pred. No. 1.6e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYKNRYRYALKSGSVNAPMPENGQTEENDWILMGSTOEAKKNAHNNRISGFSG 60
Db 573 LYKNRYRYALKSGSVNAPMPENGQTEENDWILMGSTOEAKKNAHNNRISGFSG 632

Qy 61 FFEENGKGNHGNALNLFNGKSAONRFLTGNTLNKISVTGG 104
Db 633 FFEENGKGNHGNALNLFNGKSAONRFLTGNTLNKISVTGG 676

RESULT 3
C81169
Iga-specific metalloendopeptidase (EC 3.4.24.13) NMB0700 [Imported] - *Neisseria meningitidis*
C:Species: *Neisseria meningitidis*
A:Variety: group B strain MDS5; strain 81139
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Dec-2000
R:Pettilin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Science 287, 1809-1815, 2000
A:Cross-references: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Vignani, A.; Complete genome sequence of *Neisseria meningitidis* serogroup B strain MDS5.
A:Reference number: A81000; MUID:20175755
A:Accession: C81169
A:Molecule type: DNA
A:Residues: 1-1815 <TEXT>
A:Cross-references: GB:AE002424; GB:AE002098; NID:97225923; PIDN:AAFA1117.1; PID:9722592
A:Experimental source: serogroup B, strain MDS5
R:Lombolt, H.; Poulsen, K.; Mogens, K.
MOL. Microbiol. 15, 495-506, 1995
A:Title: Comparative characterization of the iga gene encoding Iga1 protease in *Neisseria*
A:Reference number: S61314; MUID:95302961
A:Accession: S61326
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 53-548 <LOW>
A:Cross-references: EMBL:X82477; NID:9732856; PIDN:CAA57860.1; PID:9732857
C:Genetics:
A:Gene: NMB0700
C:Superfamily: Iga-specific metalloendopeptidase
C:Keywords: hydrolase; metalloproteinase

Self

Query Match 99.3%; Score 554; DB 2; Length 1815;
Best Local Similarity 99.0%; Pred. No. 4.1e-48;
Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYKNRYRYALKSGSVNAPMPENGQTEENDWILMGSTOEAKKNAHNNRISGFSG 60
Db 573 LYKNRYRYALKSGSVNAPMPENGQTEENDWILMGSTOEAKKNAHNNRISGFSG 632

Qy 61 FFEENGKGNHGNALNLFNGKSAONRFLTGNTLNKISVTGG 104
Db 633 FFEENGKGNHGNALNLFNGKSAONRFLTGNTLNKISVTGG 676

RESULT 4
A26039
Iga-specific metalloendopeptidase (EC 3.4.24.13) precursor - *Neisseria gonorrhoeae* (s
N:Alternate names: Iga protease; immunoglobulin A1 protease
C:Species: *Neisseria gonorrhoeae*
A:Variety: strain MS11
C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 08-Dec-2000
C:Accession: A26039; S09386
R:Pohlner, J.; Halter, R.; Beyreuther, K.; Meyer, T.F.
A:Title: Gene structure and extracellular secretion of *Neisseria gonorrhoeae* Iga prot
A:Reference number: A26039; MUID:87115023
A:Accession: A26039
A:Molecule type: DNA
A:Residues: 1-1532 <POH>
A:Cross-references: GB:X04835; NID:944868; PIDN:CAA28538.1; PID:944869
A:Note: the authors translated the codon AAG for residue 668 as Asn
R:Halter, R.; Pohlner, J.; Meyer, T.F.
EMBO J. 6, 2737-2744, 1989
A:Title: Mosaic-like organization of Iga protease genes in *Neisseria gonorrhoeae* gene
A:Reference number: S09386; MUID:90060036
A:Accession: S09386
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 281-325, 'N', 327-337, 'N', 339-427, 'M', 429-531, 'N', 533-615, 'V', 617-631, 'N', 6
A:Experimental source: strain MS11
C:Genetics:
A:Gene: iga
C:Superfamily: Iga-specific metalloendopeptidase
C:Keywords: hydrolase; metalloproteinase; transmembrane protein
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-153/Protein: immunoglobulin A1 proteinase #status predicted <MAT>
F:986-987/Cleavage site: Pro-Ser (autolytic) #status predicted
F:1018-1019/Cleavage site: Pro-Ser (autolytic) #status predicted
F:1121-1122/Cleavage site: Pro-Ala (autolytic) #status predicted

Query Match 87.5%; Score 488; DB 2; Length 1532;
Best Local Similarity 86.5%; Pred. No. 1.8e-41;
Matches 90; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 1 LYKNRYRYALKSGSVNAPMPENGQTEENDWILMGSTOEAKKNAHNNRISGFSG 60
Db 564 LYKNRYRYALKSGSVNAPMPENGQTEENDWILMGSTOEAKKNAHNNRISGFSG 643

Qy 61 FFEENGKGNHGNALNLFNGKSAONRFLTGNTLNKISVTGG 104
Db 644 FFEENGKGNHGNALNLFNGKSAONRFLTGNTLNKISVTGG 687

RESULT 5
A37023
Iga-specific metalloendopeptidase (EC 3.4.24.13) type 1 precursor - *Haemophilus influ*
N:Alternate names: immunoglobulin A1 proteinase type 1
C:Species: *Haemophilus influenzae*
C:Date: 31-Jan-1992 #sequence_revision 12-Jun-1992 #text_change 08-Dec-2000
C:Accession: A37023
R:Poulsen, K.; Brandt, J.; Hjorth, J.P.; Thøgersen, H.C.; Killian, M.
Infect. Immun. 57, 3097-3105, 1989

Tue May 1 15:15:37 2001

US-09-142-970-2.LDL

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 1, 2001, 14:59:28 ; Search time 37.5 Seconds
(without alignments)
53.278 Million cell updates/sec

Title: US-09-142-970-2

Perfect score: 562
Sequence: 1 LYKNNRYALKSGGSVNAP.....NRFLLTGTLNKRISVTG 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Maximum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database :

1: Issued_Patents_AA:*
2: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	505	89.9	1507	6 5268270-2	Patent No. 5268270
2	329.5	58.6	1541	5 PCT-US95-10661A-3	Sequence 3, Appli
3	322.5	57.4	1702	5 PCT-US95-10661A-5	Sequence 5, Appli
4	319.5	56.9	1545	5 PCT-US95-10661A-4	Sequence 4, Appli
5	312.5	55.6	1848	5 PCT-US95-10661A-6	Sequence 6, Appli
6	114	20.3	1394	5 PCT-US95-10661A-2	Sequence 2, Appli
7	83	13.6	1577	2 US-08-793-824-2	Sequence 2, Appli
8	76.5	13.6	631	1 US-08-487-890A-111	Sequence 111, App
9	76.5	13.6	631	2 US-08-478-435-111	Sequence 111, App
10	76.5	13.6	631	2 US-08-337-483-111	Sequence 111, App
11	76.5	13.6	631	2 US-08-478-373-111	Sequence 111, App
12	76.5	13.6	631	2 US-08-478-671-111	Sequence 111, App
13	76.5	13.6	631	3 US-08-483-577A-111	Sequence 111, App
14	74.5	13.3	430	2 US-08-945-848-8	Sequence 8, Appli
15	74.5	13.3	631	1 US-08-487-890A-115	Sequence 115, App
16	74.5	13.3	631	2 US-08-478-435-115	Sequence 115, App
17	74.5	13.3	631	2 US-08-337-483-115	Sequence 115, App
18	74.5	13.3	631	2 US-08-478-373-115	Sequence 115, App
19	74.5	13.3	631	3 US-08-474-671-115	Sequence 115, App
20	74.5	13.3	631	3 US-08-483-577A-115	Sequence 115, App
21	73.5	13.1	671	2 US-08-737-716-13	Sequence 13, Appli
22	71	12.6	708	3 US-08-613-009A-22	Sequence 22, Appli
23	71	12.6	806	1 US-07-980-528-2	Sequence 2, Appli
24	68	12.1	394	1 US-08-673-816-6	Sequence 6, Appli
25	68	12.1	648	1 US-08-487-890A-109	Sequence 109, App
26	68	12.1	648	2 US-08-478-435-109	Sequence 109, App
27	68	12.1	648	2 US-08-337-483-109	Sequence 109, App

28	68	12.1	648	2	US-08-478-373-109	Sequence 109, App
29	68	12.1	648	3	US-08-474-671-109	Sequence 109, App
30	68	12.1	648	3	US-08-483-577A-109	Sequence 109, App
31	67.5	12.0	613	1	US-08-272-875-3	Sequence 20, Appli
32	66.5	11.8	731	2	US-08-696-944-20	Sequence 3, Appli
33	66	11.7	434	2	US-08-795-475-3	Sequence 3, Appli
34	65	11.6	1529	2	US-08-728-470-10	Sequence 10, Appli
35	65	11.6	1600	2	US-08-617-697-10	Sequence 10, Appli
36	64.5	11.5	890	2	US-08-483-101-14	Sequence 14, Appli
37	64.5	11.5	1536	1	US-08-038-682-2	Sequence 2, Appli
38	64.5	11.5	1536	1	US-08-302-832-2	Sequence 2, Appli
39	64.5	11.5	1536	2	US-08-530-198-2	Sequence 2, Appli
40	64.5	11.5	1536	2	US-08-469-880-2	Sequence 2, Appli
41	64.5	11.5	1536	2	US-08-728-470-2	Sequence 2, Appli
42	64.5	11.5	1536	2	US-08-617-697-2	Sequence 2, Appli
43	64	11.4	711	3	US-08-613-009A-21	Sequence 21, Appli
44	64	11.4	1477	1	US-08-038-682-4	Sequence 4, Appli
45	64	11.4	1477	1	US-08-302-832-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
5268270-2
Patent No. 5268270
APPLICANT: Meyer, Thomas F., Halter, Roman, Pohlner, Johannes
TITLE OF INVENTION: PROCESS FOR PRODUCING PROTEINS USING GRAM
NEGATIVE HOST CELLS
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/171,872
FILING DATE: 01-JUL-1987
SEQ ID NO: 2
LENGTH: 1507
5268270-2

Query Match 89.9% Score 505. DB 6: Length 1507;
Best Local Similarity 88.5% Pred. No. 7.7e-53;
Matches 92; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 LYKNNRYALKSGGSVNAPPEGVTEENNDDWVNGYTOEAKKNNRNORISGSG 60
DB 559 LYKNNRYALKSGGSVNAPPEGVTEENNDDWVNGYTOEAKKNNRNORISGSG 60
QY 61 FFGEENGKNGALNLFNGKSAONRELLTGTLNKRISVTG 104
DB 619 FFDEENGKNGALNLFNGKSAONRELLTGTLNKRISVTG 662

RESULT 2
PCT-US95-10661A-3
Sequence 3, Application PC/TUS9510661A
GENERAL INFORMATION:
APPLICANT: Washington University, et al.
TITLE OF INVENTION: Haemophilus Adherence and Penetration Protein
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10661A
FILING DATE: 16-AUG-1995

OM protein - protein search, using sw model

Run on: May 1, 2001, 15:00:16 ; Search time 43.98 Seconds

(without alignments)
162,510 Million cell updates/sec

Title: US-09-142-970-2

Perfect score: 562

Sequence: 1 LYKNRYRYALSKSGSVNAP.....NRFLLTGTLNGKISVTG 104

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_67:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	540	96.1	1561	2 S61314	Iga-specific metal
2	540	96.1	1773	2 A81937	Iga-specific metal
3	536	95.4	1815	2 C81169	Iga-specific metal
4	508	90.4	1532	2 A26039	Iga-specific metal
5	328.5	58.6	1541	2 A37023	Iga-specific metal
6	328.5	58.5	1694	2 H64106	Iga-specific metal
7	328.5	58.5	1702	2 A41859	Iga-specific metal
8	319.5	56.9	1545	2 B41859	Iga-specific metal
9	318.5	56.7	1849	2 C41859	Iga-specific metal
10	133	23.7	1431	2 A81018	serine-type peptid
11	115.5	20.6	709	2 C64057	Iga-specific metal
12	115	20.5	1449	2 B81963	Iga-specific metal
13	114	20.3	1394	2 S60762	Iga-specific metal
14	111.5	19.8	1457	2 D81019	Iga-specific metal
15	83.5	14.9	451	2 A23535	clustered asparagi
16	83.5	14.9	465	2 S41644	polyadenylate-bind
17	83	14.8	1577	2 T30858	glycosyltransferas
18	82.5	14.7	243	2 T24981	hypothetical prote
19	77	13.7	163	2 T23076	hypothetical prote
20	77	13.7	625	2 D64107	transferrin-bindin
21	77	13.7	712	2 E81196	transferrin-bindin
22	77	13.7	982	1 A44831	phosphoenolpyruvat
23	76	13.7	1650	2 T18444	hypothetical prote
24	76	13.5	631	2 T10265	arabinogalactan-pr
25	75.5	13.4	419	2 S70908	transferrin-bindin
26	75.5	13.4	484	2 T40014	probable vesicular
27	75.5	13.4	484	2 G70846	hypothetical glyci
28	75.5	13.4	764	2 H71607	hypothetical prote
29	75	13.3	568	2 JC7210	molluscan shell ma

30	75	13.3	629	2 B75330	probable ribosomal
31	74.5	13.3	631	2 S70910	transferrin-bindin
32	74.5	13.3	719	2 S61046	ABPI protein - yea
33	74.5	13.3	1029	2 S64731	serine/threonine-s
34	74.5	13.3	1596	2 A33106	neurogenic locus m
35	74	13.2	607	2 T32968	hypothetical prote
36	74	13.2	1243	2 S07278	tall fiber protein
37	73.5	13.1	671	2 A38109	autolysin - Entero
38	72.5	12.9	642	2 D81401	probable flagellar
39	72	12.8	304	2 S65198	hypothetical prote
40	71.5	12.7	328	2 S24203	protein 1 - Neisse
41	71	12.6	402	2 T13614	N-acetyltransferas
42	71	12.6	697	2 T16306	hypothetical prote
43	71	12.6	806	2 S22765	heterogeneous ribo
44	71	12.6	2529	2 B64635	toxin-like outer m
45	70.5	12.5	125	2 T24982	hypothetical prote

ALIGNMENTS

RESULT 1
S61314
Iga-specific metalloendopeptidase (EC 3.4.24.13) homolog - Neisseria meningitidis
C:Species: Neisseria meningitidis
A:Variety: HF13
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 08-Dec-2000
C:Accession: S61314
R:Holmolt, H.; Poulsen, K.; Mogens, K.
Mol: Microbiol. 15, 495-506, 1995
A:Title: Comparative characterization of the iga gene encoding iga1 protease in Ne
A:Reference number: S61314; MUID:95302961
A:Accession: S61314
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1561 <LOW>
A:Cross-references: EMBL:X82474; NID:g732873; PIDN:CA57857.1; PID:g732874
C:Superfamily: Iga-specific metalloendopeptidase
C:Keywords: hydrolase; metalloprotease

Query Match 96.1%; Score 540; DB 2; Length 1561;
Best Local Similarity 96.2%; Pred. No. 9,2e-46;
Matches 100; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LYKNRYRYALSKSGSVNAPMPENGTEENNDAVFMKYTEEAKKNNKNNORISGSG 60
|||||
DB 584 LYKNRYRYALSKSGSVNAPMPENGTEENNDAVFMKYTEEAKKNNKNNORISGSG 643
QY 61 FFEENGKGNALNLFNGKSNONRFLTGTLNGKISVTG 104
|||||
DB 644 FFEENGKGNALNLFNGKSNONRFLTGTLNGKISVTG 687

RESULT 2
A81937
Iga-specific metalloendopeptidase (EC 3.4.24.13) NMA0905 [imported] - Neisseria me
N:Alternate names: Iga proteinase; Iga1 proteinase (EC 3.4.21.7) [misnomer]; Immun
C:Species: Neisseria meningitidis
A:Variety: group A strain Z2491; strain HF117; strain HF159; strain SM1027
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 08-Dec-2000
C:Accession: A81937; S61317; S61318; S61321
R:Parshall, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.;
Holmolt, S.; Jørgensen, K.; Leather, S.; Mungall, K.; Quail, M.A.; Rajan
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22.
A:Reference number: A81775; MUID:20222556
A:Accession: A81937
A:Molecule type: DNA
A:Residues: 1-1773 <PAR>
A:Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CA884182.1; PID:g
A:Experimental source: serogroup A, strain Z2491
R:Holmolt, H.; Poulsen, K.; Mogens, K.

Mol. Microbiol. 15, 495-506, 1995
A:Title: Comparative characterization of the iga gene encoding Iga1 protease in *Neisseria*
A:Reference number: S61314; MUID:95302961
A:Accession: S61317
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 53-548 <LOM>
A:Cross-references: EMBL:X82470; NID:9732854; PIDN:CAA57853.1; PID:9732855
A:Experimental source: strain HF117
A:Accession: S61318
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 53-548 <LOM>
A:Cross-references: EMBL:X82471; NID:9732858; PIDN:CAA57854.1; PID:9732859
A:Experimental source: strain HF159
A:Accession: S61321
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 53-548 <LOM>
A:Cross-references: EMBL:X82472; NID:9732852; PIDN:CAA57855.1; PID:9732853
A:Experimental source: strain SM1027
A:Gene: iga; NMA0905
C:Genetics:
C:Superfamily: Iga-specific metalloendopeptidase
C:Keywords: hydrolase; metalloproteinase

Seq 2

Query Match 96.1%; Score 540; DB 2; Length 1773;
Best Local Similarity 96.2%; Pred. No. 1.1e-45;
Matches 100; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 LYKKNRYVALKSGGSVNAPEPENGVTENNPMVEMGYTQDEAKKNAHKNRISGFSG 60
DB 573 LYKKNRYVALKSGGSVNAPEPENGVTENNPMVEMGYTQDEAKKNAHKNRISGFSG 632
QY 61 PFGEENGKGNALNLNFGNGSAONRFLLTGTNLNGKISVTG 104
DB 633 PFGEENGKGNALNLNFGNGSAONRFLLTGTNLNGKISVTG 676
RESULT 3
C81169
IGA-specific metalloendopeptidase (EC 3.4.24.13) NMB0700 [imported] - *Neisseria meningitidis*
C:Species: *Neisseria meningitidis*
A:Variety: group B strain M058; strain 81139
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Dec-2000
C:Accession: C81169; S61326
R:Retellin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Li, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Piazza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappunli, R.; Ve
A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain M058.
A:Reference number: A81000; MUID:20175755
A:Accession: C81169
A:Molecule type: DNA
A:Residues: 1-1815 <TEXT>
A:Cross-references: GB:AE002424; GB:AE002098; NID:97225923; PIDN:AAF41117.1; PID:9722592
A:Experimental source: serogroup B, strain MMD58
R:Lomdahl, H.; Poulsen, K.; Mogens, K.
Mol. Microbiol. 15, 495-506, 1995
A:Title: Comparative characterization of the iga gene encoding Iga1 protease in *Neisseria*
A:Reference number: S61314; MUID:95302961
A:Accession: S61326
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 53-548 <LOM>
A:Cross-references: EMBL:X82477; NID:9732856; PIDN:CAA57860.1; PID:9732857
A:Experimental source: metalloproteinase; metalloproteinase

Query Match 95.4%; Score 536; DB 2; Length 1815;
Best Local Similarity 95.2%; Pred. No. 2.7e-45;
Matches 99; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 LYKKNRYVALKSGGSVNAPEPENGVTENNPMVEMGYTQDEAKKNAHKNRISGFSG 60
DB 573 LYKKNRYVALKSGGSVNAPEPENGVTENNPMVEMGYTQDEAKKNAHKNRISGFSG 632
QY 61 PFGEENGKGNALNLNFGNGSAONRFLLTGTNLNGKISVTG 104
DB 633 PFGEENGKGNALNLNFGNGSAONRFLLTGTNLNGKISVTG 676

RESULT 4
A26039
IGA-specific metalloendopeptidase (EC 3.4.24.13) precursor - *Neisseria gonorrhoeae* (s
N:Alternate names: Iga protease; immunoglobulin A1 proteinase
C:Species: *Neisseria gonorrhoeae*
A:Variety: strain MS11
C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 08-Dec-2000
C:Accession: A26039; S09386
R:Pohlner, J.; Halter, R.; Beyreuther, K.; Meyer, T.F.
Nature 325, 458-462, 1987
A:Title: Gene structure and extracellular secretion of *Neisseria gonorrhoeae* Iga prot
A:Reference number: A26039; MUID:87115823
A:Accession: A26039
A:Molecule type: DNA
A:Residues: 1-1532 <PRO>
A:Cross-references: GB:X04835; NID:944868; PIDN:CAA28538.1; PID:944869
A:Note: the authors translated the codon AAG for residue 668 as Asn
R:Halter, R.; Pohlner, J.; Meyer, T.F.
EMBO J. 8, 2737-2744, 1989
A:Title: Mosaic-like organization of Iga protease genes in *Neisseria gonorrhoeae* gene
A:Reference number: S09386; MUID:90060036
A:Accession: S09386
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 281-325, 'N', 327-337, 'N', 339-427, 'M', 429-531, 'N', 533-615, 'V', 617-631, 'N', 6
A:Experimental source: strain MS11
C:Genetics:
A:Gene: iga
C:Superfamily: Iga-specific metalloendopeptidase
C:Keywords: hydrolase; metalloproteinase; transmembrane protein
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-1532/Product: immunoglobulin A1 proteinase #status predicted <MAT>
F:988-987/Cleavage site: Pro-Ser (autolytic) #status predicted
F:1018-1019/Cleavage site: Pro-Ser (autolytic) #status predicted
F:1121-1122/Cleavage site: Pro-Ala (autolytic) #status predicted

Query Match 90.4%; Score 508; DB 2; Length 1532;
Best Local Similarity 88.5%; Pred. No. 1.4e-42;
Matches 92; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 1 LYKKNRYVALKSGGSVNAPEPENGVTENNPMVEMGYTQDEAKKNAHKNRISGFSG 60
DB 584 LYKKNRYVALKSGGSVNAPEPENGVTENNPMVEMGYTQDEAKKNAHKNRISGFSG 643
QY 61 PFGEENGKGNALNLNFGNGSAONRFLLTGTNLNGKISVTG 104
DB 644 PFGEENGKGNALNLNFGNGSAONRFLLTGTNLNGKISVTG 687
RESULT 5
A37023
IGA-specific metalloendopeptidase (EC 3.4.24.13) type 1 precursor - *Haemophilus influ*
N:Alternate names: immunoglobulin A1 proteinase type 1
C:Species: *Haemophilus influenzae*
C:Date: 31-Jan-1992 #sequence_revision 12-Jun-1992 #text_change 08-Dec-2000
C:Accession: A37023
R:Poulsen, K.; Brandt, J.; Hjorth, J.P.; Thøgersen, H.C.; Kilian, M.
Infect. Immun. 57, 3097-3105, 1989

OM protein - protein search, using sw model

Run on: May 1, 2001, 14:59:29 ; Search time 37.5 Seconds
(without alignments)

53.278 Million cell updates/sec

Title: US-09-142-970-3

Perfect score: 563
1 LYXKNRYALKSGSVNAP.....NRELLGGINLNGKISVTQG 104

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	492	87.4	1507	5268270-2	Patent No. 5268270
2	326.5	58.0	1545	PCT-US95-10661A-4	Sequence 4, Appl
3	320.5	56.9	1541	PCT-US95-10661A-3	Sequence 3, Appl
4	313.5	55.7	1702	PCT-US95-10661A-5	Sequence 5, Appl
5	303.5	53.9	1848	PCT-US95-10661A-6	Sequence 6, Appl
6	114	20.2	1394	PCT-US95-10661A-2	Sequence 2, Appl
7	78.5	13.6	430	US-08-945-848-8	Sequence 8, Appl
8	78	13.9	1577	US-08-793-824-2	Sequence 2, Appl
9	73.5	13.1	806	US-07-980-528-2	Sequence 2, Appl
10	71	12.6	394	US-08-673-814-6	Sequence 6, Appl
11	70.5	12.5	631	US-08-487-890A-115	Sequence 115, App
12	70.5	12.5	631	US-08-478-435-115	Sequence 115, App
13	70.5	12.5	631	US-08-337-483-115	Sequence 115, App
14	70.5	12.5	631	US-08-478-373-115	Sequence 115, App
15	70.5	12.5	631	US-08-478-373-115	Sequence 115, App
16	70.5	12.5	631	US-08-478-373-115	Sequence 115, App
17	67.5	12.0	671	US-08-737-716-13	Sequence 13, Appl
18	66.5	11.8	890	US-08-483-101-14	Sequence 14, Appl
19	66.5	11.8	936	PCT-US93-05944-2	Sequence 2, Appl
20	65	11.5	648	US-08-487-890A-109	Sequence 109, App
21	65	11.5	648	US-08-478-435-109	Sequence 109, App
22	65	11.5	648	US-08-337-483-109	Sequence 109, App
23	65	11.5	648	US-08-478-373-109	Sequence 109, App
24	65	11.5	648	US-08-478-373-109	Sequence 109, App
25	65	11.5	648	US-08-483-577A-109	Sequence 109, App
26	65	11.5	1338	US-08-128-470-9	Sequence 9, Appl
27	65	11.5	1599	US-08-617-697-9	Sequence 9, Appl

28	64.5	11.5	631	1	US-08-487-890A-111	Sequence 111, App
29	64.5	11.5	631	2	US-08-478-435-111	Sequence 111, App
30	64.5	11.5	631	2	US-08-337-483-111	Sequence 111, App
31	64.5	11.5	631	2	US-08-478-373-111	Sequence 111, App
32	64.5	11.5	631	3	US-08-478-671-111	Sequence 111, App
33	64.5	11.5	631	3	US-08-483-577A-111	Sequence 111, App
34	64.5	11.5	691	1	US-08-064-174-2	Sequence 2, Appl
35	64.5	11.5	691	1	US-08-066-167-4	Sequence 4, Appl
36	64.5	11.5	691	2	US-08-449-733-2	Sequence 2, Appl
37	64.5	11.5	692	1	US-08-448-194-62	Sequence 62, Appl
38	64.5	11.5	711	1	US-08-487-890A-98	Sequence 98, Appl
39	64.5	11.5	711	2	US-08-478-435-98	Sequence 98, Appl
40	64.5	11.5	711	2	US-08-337-483-98	Sequence 98, Appl
41	64.5	11.5	711	2	US-08-478-373-98	Sequence 98, Appl
42	64.5	11.5	711	3	US-08-474-671-98	Sequence 98, Appl
43	64.5	11.5	711	3	US-08-483-577A-98	Sequence 98, Appl
44	64.5	11.5	711	3	US-08-448-194-8	Sequence 8, Appl
45	64	11.4	546	2	US-08-942-423-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
Patent No. 5268270
APPLICANT: Meyer, Thomas F.; Halter, Roman; Pohlner, Johannes
TITLE OF INVENTION: PROCESS FOR PRODUCING PROTEINS USING GRAM
NEGATIVE HOST CELLS
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/171, 872
FILING DATE: 01-JUL-1987
SEQ ID NO: 2:
LENGTH: 1507
5268270-2

Query Match 87.4% Score 492; DB 6; Length 1507;
Best Local Similarity 86.5%; Pred. No. 2.9e-51;
Matches 90; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 LYXKNRYALKSGSVNAPMPENGQTEENNDFVFMGKQDEAKNKNRNRISFGSG 60
DB 559 LYXKNRYALKSGSVNAPMPENGQTEENNDFVFMGKQDEAKNKNRNRISFGSG 618
QY 61 PGEENGKGNALNENKSAONRFLITGTNTNGKISVTQG 104
DB 619 PGEENGKGNALNENKSAONRFLITGTNTNGKISVTQG 662
RESULT 2
PCT-US95-10661A-4
GENERAL INFORMATION:
SEQUENCE 4, Application PC/TUS9510661A
APPLICANT: Washington University, et al.
TITLE OF INVENTION: Haemophilus Adherence and Penetration Protein
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Flehr, Holbach, Test, Albitton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10661A
FILING DATE: 16-AUG-1995

OM protein - protein search, using sw model

Run on: May 1, 2001, 15:00:17 ; Search time 43.98 Seconds
(without alignments)
162.510 Million cell updates/sec

Title: US-09-142-970-3

Perfect score: 563
Sequence: 1 LYKKNRYVALKSGSVNAP.....NRFLLTGCTNLNKISVTG 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Maximum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_67: **
1: pir1: **
2: pir2: **
3: pir3: **
4: pir4: **

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	537	95.4	1561	2 S61314	Iga-specific metal
2	537	95.4	1773	2 A81937	Iga-specific metal
3	533	94.7	1815	2 C81169	Iga-specific metal
4	495	87.9	1532	2 A26039	Iga-specific metal
5	326.5	58.0	1345	2 B41859	Iga-specific metal
6	320.5	56.9	1541	2 A37023	Iga-specific metal
7	319.5	56.7	1694	2 H64106	Iga-specific metal
8	319.5	56.7	1702	2 A41859	Iga-specific metal
9	309.5	55.0	1849	2 C41859	Iga-specific metal
10	132	23.4	1431	2 A81018	serine-type peptid
11	114	20.2	1394	2 S60762	Iga-specific serin
12	113.5	20.2	709	2 C64057	Iga-specific metal
13	112.5	20.0	1449	2 B81963	Iga-specific serin
14	109	19.4	1457	2 D81019	adhesion and penet
15	86.5	15.4	4451	2 A23535	clustered asparagi
16	80	14.2	163	2 T23076	hypothetical prote
17	80	14.2	2529	2 B64635	toxin-like outer m
18	79	14.0	179	2 T20206	hypothetical prote
19	79	14.0	402	2 T13614	N-acetyltransferas
20	79	14.0	629	2 B75330	probable ribosomal
21	79	14.0	1650	2 T18444	hypothetical prote
22	79	14.0	2399	2 H71879	toxin-like outer m
23	78	13.9	461	2 T10265	arabinogalactan-pr
24	78	13.9	568	2 JC7210	molluscan shell ma
25	78	13.9	625	2 D64107	transferrin-binding
26	78	13.9	1243	2 S07278	tail fiber protein
27	78	13.9	1577	2 T30858	glucosyltransferas
28	76.5	13.6	243	2 T24961	hypothetical prote
29	76.5	13.6	419	2 T40014	probable vesicular

30	76.5	13.6	954	1 S20907
31	76.5	13.6	1029	2 S64731
32	75.5	13.4	465	2 S45644
33	75.5	13.4	484	2 G70846
34	75	13.3	697	2 T16306
35	74.5	13.2	1596	2 A33106
36	74	13.1	698	2 JH0163
37	74	13.1	700	2 JH0162
38	74	13.1	982	1 A44831
39	74	13.1	1449	2 T30857
40	73.5	13.1	350	2 T06689
41	73.5	13.1	806	2 S22765
42	73	13.0	537	2 A23770
43	73	13.0	1449	2 T30552
44	72.5	12.9	364	2 S43574
45	72.5	12.9	694	1 DNCHNL

ALIGNMENTS

RESULT 1
S61314
Iga-specific metalloendopeptidase (EC 3.4.24.13) homolog - Neisseria meningitidis
C:Species: Neisseria meningitidis
A:Variety: HP13
C:Date: 20-Jul-1996 #sequence-revision 13-Mar-1997 #text-change 08-Dec-2000
C:Accession: S61314
R: Lomholt, H.; Poulsen, K.; Mogens, K.
Mol. Microbiol. 15, 495-506, 1995
A:Title: Comparative characterization of the iga gene encoding Iga1 protease in Neiss
A:Reference number: S61314; M01D:95302961
A:Accession: S61314
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1561 <L0M>
A:Cross-references: EMBL:X82474; NID:g732873; PIDN:CA57857.1; PID:g732874
C:Superfamily: Iga-specific metalloendopeptidase
C:Keywords: hydrolase; metalloproteinase

Query Match 95.4% Score 537; DB 2; Length 1561;
Best Local Similarity 95.2% Pred. No. 1.2e+45;
Matches 99; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 LYKKNRYVALKSGSVNAPMPENGTENNDFVNGYKQEAQKAMNKNORISGFG 60
|||||
DB 584 LYKKNRYVALKSGSVNAPMPENGTENNDFVNGYKQEAQKAMNKNORISGFG 643
QY 61 FFEENKGNHGNALNLFNGSKAQNREPLTGTNLNKGISVTG 104
|||||
DB 644 FFEENKGNHGNALNLFNGSKAQNREPLTGTNLNKGISVTG 687

RESULT 2
A81937
Iga-specific metalloendopeptidase (EC 3.4.24.13) NMA0905 [imported] - Neisseria mening
N:Alternate names: Iga1 protease; Iga1 protease (EC 3.4.21.7) [misomer]; immunog
C:Species: Neisseria meningitidis
A:Variety: group A strain Z2491; strain HP117; strain HP159; strain SM1027
C:Date: 05-May-2000 #sequence-revision 05-May-2000 #text-change 08-Dec-2000
C:Accession: A81937; S61317; S61318; S61321
R: Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churher, C.; Klee, S.R.; Mo
R: Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 400, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
A:Reference number: A81775; M01D:2022356
A:Accession: A81937
A:Molecule type: DNA
A:Residues: 1-1773 <PAR>
A:Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CA84182.1; PID:g737
A:Experimental source: serogroup A, strain Z2491
R: Lomholt, H.; Poulsen, K.; Mogens, K.

OM protein - protein search, using sw model

Run on: May 1, 2001, 15:03:35 ; Search time 26.69 seconds

(Without alignments)
133,480 Million cell updates/sec

Title: US-09-142-970-3

Sequence: 1 LYKNRYRYALKSGGSVNAPNRFLLTGSTNLNGKISVNOG 104

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	495	87.9	1532	1	IGA_NEIGO
2	326.5	58.0	1545	1	IGA3_HAEIN
3	320.5	56.9	1541	1	IGA1_HAEIN
4	319.5	56.7	1594	1	IGA2_HAEIN
5	319.5	56.7	1702	1	IGA2_HAEIN
6	309.5	55.0	1849	1	IGA4_HAEIN
7	114	20.2	1394	1	HAP_HAEIN
8	113.5	20.2	1409	1	HAP1_HAEIN
9	95.5	17.0	989	1	PTP3_DICDI
10	86.5	15.4	451	1	ARP2_PLAFA
11	78	13.9	625	1	TBP2_HAEIN
12	76.5	13.6	1243	1	VG37_BPK3
13	76.5	13.6	954	1	XYNA_RUMFL
14	74.5	13.2	1029	1	KSP1_YEAST
15	74.5	13.2	1596	1	MAM_DROME
16	74	13.1	700	1	NOMA_DROME
17	74	13.1	982	1	CASP_ANASP
18	73.5	13.1	824	1	ROU_HUMAN
19	73	13.0	537	1	ARP_PLAFA
20	72.5	12.9	401	1	KO3_CAEEL
21	72.5	12.9	694	1	NUCL_CHICK
22	72.5	12.9	719	1	ARP_YEAST
23	72	12.8	563	1	SRB8_CHICK
24	71	12.6	417	1	Y943_MERJA
25	70.5	12.4	507	1	VLI_HPV09
26	70	12.4	550	1	SRB8_HUMAN
27	70	12.4	712	1	TBPB_NEIMB
28	69.5	12.3	2334	1	WAPA_BACSU
29	69.5	12.3	882	1	IF2_BORBU
30	69	12.3	1113	1	N116_YEAST
31	68.5	12.2	606	1	MANA_PIRSP
32	67.5	12.0	671	1	ALYS_ENTFA
33	67.5	12.0	1902	1	P2P_LACPA

Seq 3

ALIGNMENTS

34	67	11.9	368	1	YB11_YEAST
35	67	11.9	546	1	SRB8_MOUSE
36	67	11.9	671	1	HMOG_DROME
37	67	11.9	685	1	ERF2_YEAST
38	67	11.9	794	1	YB52_MYCPN
39	66.5	11.8	716	1	PEP_DROME
40	66	11.7	604	1	DED1_YEAST
41	65.5	11.6	469	1	K1CX_HUMAN
42	65	11.5	361	1	APBA_DICDI
43	65	11.5	464	1	DNAA_TREPA
44	65	11.5	1556	1	GLTS_SYNZ3
45	64.5	11.5	623	1	PNT1_DROME

RESULT	1	STANDARD	PRT	1532 AA.
IGA_NEIGO				
ID	IGA_NEIGO			
AC	P09790;			
DT	01-MAR-1989 (Rel. 10, Created)			
DT	01-MAR-1989 (Rel. 10, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	IGA-SPECIFIC SERINE ENDOPEPTIDASE PRECURSOR (EC 3.4.21.72) (IGA PROTEASE).			
GN	IGA.			
OS	Neisseria gonorrhoeae.			
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.			
OX	NCBI_Taxid=485;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	STRAIN=MS11;			
RA	MEDLINE=87115823; PubMed=3021577;			
FX	Pohlner J., Halter R., Beyreuther K., Meyer T.F.;			
RT	"Gene structure and extracellular secretion of Neisseria gonorrhoeae IGA protease."			
RL	Nature 325:458-462(1987).			
RP	ACTIVE SITE.			
RX	MEDLINE=90154052; PubMed=2105953;			
RA	Bachovchin W.W., Plant A.G., Flentke G.R., Lynch M., Kettner C.A.;			
RT	"Inhibition of Iga1 proteinases from Neisseria gonorrhoeae and Hemophilus influenzae by peptide prolyl boronic acids."			
RL	J. Biol. Chem. 265:3738-3743(1990).			
CC	- FUNCTION: THIS PROTEASE IS SPECIFIC FOR IMMUNOGLOBULIN A.			
CC	- CATALYTIC ACTIVITY: CLEAVAGE OF IMMUNOGLOBULIN A MOLECULES AT CERTAIN PRO-1-XAA BONDS IN THE HINGE REGION. NO SMALL MOLECULE SUBSTRATES ARE KNOWN.			
CC	- SUBCELLULAR LOCATION: SECRETED.			
CC	- DOMAIN: THE SIGNAL PEPTIDE GUIDE THE PRECURSOR TO THE PERIPLASMIC SPACE, AND THE CARBOXY-TERMINAL HELPER DOMAIN ASSOCIATES WITH THE OUTER MEMBRANE TO FORM A PORE FOR EXCRETION OF THE PROTEASE			
CC	DOMAIN. THE HELPER DOMAIN IS THEN RELEASED BY AUTOPROTEOLYSIS.			
CC	- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S6 (SERINE PROTEASE).			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
DR	EMBL; X04835; CAA28538.1;			
DR	PIR; A26039; A26039.			
DR	MEROPS; S06.001;			
DR	InterPro; IPR000710;			
DR	PRINTS; PR00921; IGASERPTASE.			
KW	Hydrolase; Serine protease; Zymogen; Autocatalytic cleavage;			
KW	Transmembrane; Signal.			
FT	SIGNAL 1 27			
FT	CHAIN 28 966			
FT	IGA-SPECIFIC SERINE ENDOPEPTIDASE.			

FT PROPEP 987 1532 HELPER PEPTIDE.
FT ACT_SITE 278 278 POTENTIAL.
FT SITE 986 987 CLEAVAGE (AUTO-).
FT SITE 1018 1019 CLEAVAGE (AUTO-).
FT SITE 1121 1122 CLEAVAGE (AUTO-).
SQ SEQUENCE 1532 AA: 168976 MW: 68FP4112BD22FC40D CRC64:

Query Match 87.9%; Score 495; DB 1; Length 1532;
Best Local Similarity 86.5%; Pred. No. 1.8e-41;
Matches 90; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

OY 1 LYKRYRYALKSGSVNAPMPENGOTENDWPMGKOEBAOKNANHNKORISFG 60
|||||
DB 584 LYKRYRYALKSGSRINAPMPENGVAENNDWIFMGYTOEARKNANHNKRRIGDFG 643
|||||
DB 644 FEDENGKNGHNGALNLFNGKSAQNRFLTGTLNGKISVTG 104
|||||

RESULT 2
ID IGAL_HAEIN STANDARD; PRT: 1545 AA.
AC P4385;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (EC 3.4.21.72) (IGAL PROTEASE).
GN IGA.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OX Haemophilus.
NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HK393 / NCTC 8467 / SEROTYPE B;
RX MEDLINE-92234949; PubMed-1373717;
RA Poulsen K., Reinholdt J., Kilian M.;
RT "A comparative genetic study of serologically distinct Haemophilus influenzae type 1 immunoglobulin A1 proteases.";
RL J. Bacteriol. 174:2913-2921(1992).
CC -1- FUNCTION: VIRULENCE FACTOR; CLEAVES HOST IMMUNOGLOBULIN A
PRODUCING INTACT FC AND FAB FRAGMENTS.
CC -1- CATALYTIC ACTIVITY: CLEAVAGE OF IMMUNOGLOBULIN A MOLECULES AT
CERTAIN PRO-1-XAA BONDS IN THE HINGE REGION. NO SMALL MOLECULE
SUBSTRATES ARE KNOWN.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- DOMAIN: THE SIGNAL PEPTIDE GUIDES THE PRECURSOR TO THE PERIPLASMIC
SPACE, AND THE CARBOXY-TERMINAL HELPER DOMAIN ASSOCIATES WITH THE
OUTER MEMBRANE TO FORM A PORE FOR EXCRETION OF THE PROTEASE
DOMAIN. THE HELPER DOMAIN IS THEN RELEASED BY AUTOPROTEOLYSIS (BY
SIMILARITY). BELONGS TO PEPTIDASE FAMILY S6 (SERINE PROTEASE).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S6 (SERINE PROTEASE).
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL: M87490: AAA24967.1; -
CC
CC MEROPS: S06.001;
CC InterPro: IPR000710; -
CC PRINTS: PR00921; IGASERPTASE.
CC HYDROLASE; Serine protease; Transmembrane; zymogen; signal.
FT CHAIN 1 25
FT SIGNAL 1 25
FT PROPEP 1013 1545
FT SIGNAL 292 292
FT CHAIN 1545 AA: 170627 MW: 3EDD753988F6D478 CRC64:

Query Match 58.0%; Score 326.5; DB 1; Length 1545;
Best Local Similarity 57.5%; Pred. No. 1e-24; Indels 3; Gaps 2;
Matches 61; Conservative 19; Mismatches 23;

OY 1 LYKRYRYALKSGSVNAPMPENGOTENDWPMGKOEBAOKNANHNKORISFG 58
|||||
DB 597 LYKRYRYALKSGSRINAPMPENGVAENNDWIFMGYTOEARKNANHNKRRIGDFG 656
|||||
DB 657 NGYFGEERK-NNGNINLVTEFKRSEONRFLTGTLNGDLNVOQG 701
|||||

RESULT 3
ID IGAL_HAEIN STANDARD; PRT: 1541 AA.
AC P42782;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (EC 3.4.21.72) (IGAL PROTEASE).
GN IGA.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OX Haemophilus.
NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HK368 / SEROTYPE B;
RX MEDLINE-89379374; PubMed-2506130;
RA Poulsen K., Brandt J., Hjorth J.P., Thøgersen H.C., Kilian M.;
RT "Cloning and sequencing of the immunoglobulin A1 protease gene (iga) of Haemophilus influenzae serotype b.";
RL Infect. Immun. 57:3097-3105(1989).
RN [2]
RP MTAGENESIS OF SER-288.
RC STRAIN-HK368 / SEROTYPE B;
RX MEDLINE-92234949; PubMed-1373717;
RA Poulsen K., Reinholdt J., Kilian M.;
RT "A comparative genetic study of serologically distinct Haemophilus influenzae type 1 immunoglobulin A1 proteases.";
RL J. Bacteriol. 174:2913-2921(1992).
CC -1- FUNCTION: VIRULENCE FACTOR; CLEAVES HOST IMMUNOGLOBULIN A
PRODUCING INTACT FC AND FAB FRAGMENTS.
CC -1- CATALYTIC ACTIVITY: CLEAVAGE OF IMMUNOGLOBULIN A MOLECULES AT
CERTAIN PRO-1-XAA BONDS IN THE HINGE REGION. NO SMALL MOLECULE
SUBSTRATES ARE KNOWN.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- DOMAIN: THE SIGNAL PEPTIDE GUIDES THE PRECURSOR TO THE PERIPLASMIC
SPACE, AND THE CARBOXY-TERMINAL HELPER DOMAIN ASSOCIATES WITH THE
OUTER MEMBRANE TO FORM A PORE FOR EXCRETION OF THE PROTEASE
DOMAIN. THE HELPER DOMAIN IS THEN RELEASED BY AUTOPROTEOLYSIS (BY
SIMILARITY). BELONGS TO PEPTIDASE FAMILY S6 (SERINE PROTEASE).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S6 (SERINE PROTEASE).
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL: X64357: CAA45708.1; -
CC EMBL: M87492: AAA24969.1; -
CC MEROPS: S06.001;
CC InterPro: IPR000710; -
CC PRINTS: PR00921; IGASERPTASE.
CC HYDROLASE; Serine protease; Transmembrane; zymogen; signal.
FT CHAIN 1 25
FT SIGNAL 26 1008
FT CHAIN 1008

OM protein - protein search, using sw model

Run on: May 1, 2001, 14:59:30 ; Search time 37.5 Seconds
(without alignments)
53.278 Million cell updates/sec

Title: US-09-142-970-4

Perfect score: 569
Sequence: 1 LYKNNRYRYALKSGRLNAP.....NRFLLTGANLNGNGRPPVK 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	520	91.4	1507	6	Patent No. 5268270
2	281.5	49.5	1561	5	PCT-US95-10661A-3
3	275.5	48.4	1702	5	PCT-US95-10661A-5
4	270.5	47.5	1545	5	PCT-US95-10661A-4
5	264.5	46.5	1848	5	PCT-US95-10661A-6
6	91	16.0	1394	5	PCT-US95-10661A-2
7	76	13.4	1577	2	US-08-793-824-2
8	74.5	13.1	631	1	US-08-487-890A-115
9	74.5	13.1	631	2	US-08-478-435-115
10	74.5	13.1	631	2	US-08-337-483-115
11	74.5	13.1	631	2	US-08-478-373-115
12	74.5	13.1	631	3	US-08-474-671-115
13	74.5	13.1	631	3	US-08-483-577A-115
14	71	12.5	430	2	US-08-945-848-8
15	68.5	12.0	605	1	US-08-462-884A-3
16	68.5	12.0	605	1	US-08-461-881B-3
17	68.5	12.0	605	2	US-09-123-960-3
18	67.5	11.9	631	1	US-08-487-890A-111
19	67.5	11.9	631	2	US-08-478-435-111
20	67.5	11.9	631	2	US-08-337-483-111
21	67.5	11.9	631	2	US-08-478-373-111
22	67.5	11.9	631	3	US-08-474-671-111
23	67.5	11.9	631	3	US-08-483-577A-111
24	66.5	11.7	759	2	US-08-450-351-2
25	66.5	11.7	759	2	US-08-450-351-4
26	66.5	11.7	759	2	US-08-323-477-2
27	65	11.4	265	3	US-08-483-577A-158

28	65	11.4	310	3	US-08-483-577A-157	Sequence 157, App
29	65	11.4	365	3	US-08-483-577A-156	Sequence 156, App
30	65	11.4	404	3	US-08-483-577A-155	Sequence 155, App
31	65	11.4	417	3	US-08-483-577A-154	Sequence 154, App
32	65	11.4	430	3	US-08-483-577A-153	Sequence 153, App
33	65	11.4	430	3	US-08-483-577A-152	Sequence 152, App
34	65	11.4	463	3	US-08-483-577A-151	Sequence 151, App
35	65	11.4	529	3	US-08-483-577A-150	Sequence 150, App
36	65	11.4	547	3	US-08-483-577A-149	Sequence 149, App
37	65	11.4	647	3	US-08-483-577A-148	Sequence 148, App
38	65	11.4	660	1	US-08-487-890A-8	Sequence 10, App1
39	65	11.4	660	1	US-08-487-890A-10	Sequence 10, App1
40	65	11.4	660	2	US-08-478-435-8	Sequence 10, App1
41	65	11.4	660	2	US-08-478-435-10	Sequence 10, App1
42	65	11.4	660	2	US-08-337-483-8	Sequence 8, App1
43	65	11.4	660	2	US-08-337-483-10	Sequence 10, App1
44	65	11.4	660	2	US-08-478-373-8	Sequence 8, App1
45	65	11.4	660	2	US-08-478-373-10	Sequence 10, App1

ALIGNMENTS

RESULT 1
5268270-2
Patent No. 5268270
APPLICANT: Meyer, Thomas F.; Halter, Roman; Pohlner, Johannes
TITLE OF INVENTION: PROCESS FOR PRODUCING PROTEINS USING GRAM
NEGATIVE HOST CELLS
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/171,872
FILING DATE: 01-JUL-1987
SEQ ID NO: 2
LENGTH: 1507
5268270-2

Query Match 91.4%; Score 520; DB 6; Length 1507;
Best Local Similarity 88.4%; Pred. No. 2.5e-52;
Matches 99; Conservative 2; Mismatches 1; Indels 10; Gaps 2;

QY 1 LYKNNRYRYALKSGRLNAPMPENGVAENNDRYFQYTOEAKKMMNNKRRIDDEG 60
DB 559 LYKNNRYRYALKSGRLNAPMPENGVAENNDRYFQYTOEAKKMMNNKRRIDDEG 618
QY 61 FPDENGKGHNGALNLFNGKSAQNRFLLTGANLNG-----GN-----GRP 102
DB 619 FPDENGKGHNGALNLFNGKSAQNRFLLTGANLNGKISYTOGNVLLSGRP 670

RESULT 2
PCT-US95-10661A-3
Sequence 3, Application PCT/US9510661A
GENERAL INFORMATION:
APPLICANT: Washington University, et al.
TITLE OF INVENTION: Haemophilus Adherence and Penetration Protein
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fleury, Hobbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10661A
FILING DATE: 16-AUG-1995

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 1, 2001, 15:00:20 ; Search time 43.98 Seconds
(without alignments)
162.510 Million cell updates/sec

Title: US-09-142-970-5
Perfect score: 565
Sequence: 1 LYNNRYRYALKSGRLNAP.....NRFLLTGANLNKISVTG 104

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues
Total number of hits satisfying chosen parameters: 198801

Maximum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	559	98.9	1532	2 A26039	Iga-specific metal
2	494	87.4	1561	2 S61314	Iga-specific metal
3	494	87.4	1773	2 A81937	Iga-specific metal
4	490	86.7	1815	2 C81169	Iga-specific metal
5	298.5	52.8	1341	2 A37023	Iga-specific metal
6	297.5	52.7	1694	2 H64106	Iga-specific metal
7	291.5	51.6	1545	2 A41859	Iga-specific metal
8	287.5	50.9	1545	2 C41859	Iga-specific metal
9	132	23.4	1431	2 A81018	Iga-specific metal
10	101	17.9	1394	2 S60762	Iga-specific metal
11	99.5	17.6	1457	2 D81019	Iga-specific metal
12	98.5	17.4	709	2 C64057	Iga-specific metal
13	94.5	16.7	1449	2 B81563	Iga-specific metal
14	76	13.5	629	2 B75330	Iga-specific metal
15	75	13.3	461	2 T10265	Iga-specific metal
16	74.5	13.2	451	2 A23535	Iga-specific metal
17	74	13.1	163	2 T27368	Iga-specific metal
18	73.5	13.0	1596	2 A33106	Iga-specific metal
19	72	12.7	419	2 T18420	Iga-specific metal
20	71	12.6	1029	2 S64731	Iga-specific metal
21	70.5	12.3	1577	2 T30858	Iga-specific metal
22	69.5	12.3	641	2 S57236	Iga-specific metal
23	69.5	12.3	958	2 A82583	Iga-specific metal
24	69.5	12.3	1436	2 S57238	Iga-specific metal
25	69.5	12.3	1449	2 S57237	Iga-specific metal
26	69.5	12.3	1436	2 S57238	Iga-specific metal
27	69.5	12.3	1436	2 S57238	Iga-specific metal
28	69.5	12.3	1436	2 S57238	Iga-specific metal
29	69.5	12.3	1436	2 S57238	Iga-specific metal

30	68.5	12.1	402	2 B82418	hypothetical prote
31	68.5	12.1	406	2 D64934	hypothetical prote
32	68.5	12.1	604	2 S39885	forked protein - f
33	68.5	12.1	1247	2 E71616	hypothetical prote
34	68.5	12.0	549	2 T20720	hypothetical prote
35	68	12.0	631	2 S70908	transferrin-blidin
36	68	12.0	643	2 S28293	hypothetical prote
37	68	12.0	730	2 S28294	hypothetical prote
38	68	12.0	1336	2 T18288	hypothetical prote
39	68	12.0	1651	2 UC1340	ABC transport prot
40	68	12.0	2529	2 B64635	outer membrane pro
41	67.5	11.9	465	2 S41644	toxlin-like outer m
42	67.5	11.9	537	2 A23770	polyadenylate-bind
43	67.5	11.9	612	2 A34967	asparagine-rich pr
44	67.5	11.9	642	2 D81401	sterol esterase (E
45	67.5	11.9	764	2 H71607	probable flagellar
					hypothetical prote

ALIGNMENTS

RESULT 1
A26039
Iga-specific metalloendopeptidase (EC 3.4.24.13) precursor - Neisseria gonorrhoeae (s
N:Alternate names: Iga protease; immunoglobulin A1 proteinase
C:Species: Neisseria gonorrhoeae
A:Variety: strain MS11
C:Date: 05-Oct-1988 #sequence_revision: 05-Oct-1988 #text_change: 08-Dec-2000
A:Accession: A26039; S09386
R:Polmer, J.; Halter, R.; Beyreuther, K.; Meyer, T.F.
Nature 325, 458-462, 1987
A:Title: Gene structure and extracellular secretion of Neisseria gonorrhoeae Iga prot
A:Reference number: A26039; MUID: 87115823
A:Accession: A26039
A:Molecule type: DNA
A:Residues: 1-1532 [POH]
A:Cross-references: GB:X04835; NID:944868; PIDN:CAA28538.1; PID:944869
A>Note: the authors translated the codon AAG for residue 668 as Asn
R:Halter, R.; Polmer, J.; Meyer, T.F.
EMBO J. 8, 2737-2744, 1989
A:Title: Mosaic-like organization of Iga protease genes in Neisseria gonorrhoeae gene
A:Reference number: S09386; MUID: 90060036
A:Accession: S09386
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 281-325, 'N', 327-337, 'N', 339-427, 'M', 429-531, 'N', 533-615, 'V', 617-631, 'N', 6
A:Experimental source: strain MS11
C:Genetics:
A:Gene: Iga
C:Superfamily: Iga-specific metalloendopeptidase
C:Keywords: hydrolase; metalloproteinase; transmembrane protein
F:1-27/Domain: signal sequence #status predicted <MAT>
F:28-1532/Product: immunoglobulin A1 proteinase #status predicted
F:986-987/Cleavage site: Pro-Ser (autolytic) #status predicted
F:1018-1019/Cleavage site: Pro-Ser (autolytic) #status predicted
F:1121-1122/Cleavage site: Pro-Ala (autolytic) #status predicted

Query Match
Best Local Similarity 98.9%
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	LYNNRYRYALKSGRLNAPPEGVAFNNDWTFMGVTOEARKNANNHNNRIGDFG 60
DB	584	LYNNRYRYALKSGRLNAPPEGVAFNNDWTFMGVTOEARKNANNHNNRIGDFG 643
QY	61	FEDENGKNGHNGALNPNFGSKAONRFLTGANLNKISVTG 104
DB	644	FEDENGKNGHNGALNPNFGSKAONRFLTGANLNKISVTG 687
RESULT	2	
		S61314

DE IGAI PROTEASE PRECURSOR (FRAGMENT).
GN IGA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN (1)
RP SEQUENCE FROM N.A.
RA Morelli G., Malorny B., Mueller K., Seiler A., Wang J., del Valle J.,
RA Achtmann M.;
RT "Clonal descent and microevolution of Neisseria meningitidis during 30
RT years of epidemic spread."
RL Mol. Microbiol. 25:1047-1064(1997).
DR EMBL; AF012204; AAC45787.1; -
DR INTERPRO; IPR000710; -
DR INTERPRO; IPR002195; -
DR PRINTS; PR00921; IGASERPTASE.
DR PROSITE; PS00482; DIHYDROOROTASE_1; UNKNOWN_1.
KM Protease.
FT NON_TER 1 1
FT 992 992
SQ SEQUENCE 992 AA; 109239 MW; 9ED0A41019917CE3 CRC64;

Query Match 87.4%; Score 494; DB 2; Length 992;
Best Local Similarity 87.5%; Pred. No. 1e-43;
Matches 91; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
OY 1 LYKRYRYALKSGRLNAPMPENGVAENNDWIFMGYTOEARKNANMKNRRIGDFGG 60
DB 557 LYKRYRYALKSGSVNAPMPENGQTEENDWILMGSTOEAKKNANMKNRRIGSGSG 616
OY 61 FFDEENGKNGALNLFNGKSAQNRFLLTGANLNGKISVTGG 104
DB 617 FFGEENGKNGALNLFNGKSAQNRFLLTGTLNKGISVTGG 660

Seq 5

RESULT 9
O30575 PRELIMINARY; PRT; 997 AA.
AC O30575;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE IGAI PROTEASE PRECURSOR (FRAGMENT).
GN IGA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE-98010345; PubMed-9350862;
RA Morelli G., Malorny B., Mueller K., Seiler A., Wang J., F.,
RA del Valle J.;
RT "Clonal descent and microevolution of Neisseria meningitidis during 30
RT years of epidemic spread."
RL Mol. Microbiol. 25:1047-1064(1997).
DR EMBL; AF012210; AAC45793.1; -
DR INTERPRO; IPR000710; -
DR INTERPRO; IPR002195; -
DR PRINTS; PR00921; IGASERPTASE.
DR PROSITE; PS00482; DIHYDROOROTASE_1; UNKNOWN_1.
KM Protease.
FT NON_TER 1 1
FT 997 997
SQ SEQUENCE 997 AA; 110152 MW; 4DEA0DE594B5E28E CRC64;

Query Match 87.4%; Score 494; DB 2; Length 997;
Best Local Similarity 87.5%; Pred. No. 1e-43;
Matches 91; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
OY 1 LYKRYRYALKSGRLNAPMPENGVAENNDWIFMGYTOEARKNANMKNRRIGDFGG 60
DB 557 LYKRYRYALKSGSVNAPMPENGQTEENDWILMGSTOEAKKNANMKNRRIGSGSG 616
OY 61 FFDEENGKNGALNLFNGKSAQNRFLLTGANLNGKISVTGG 104
DB 617 FFGEENGKNGALNLFNGKSAQNRFLLTGTLNKGISVTGG 660

DB 558 LYKRYRYALKSGSVNAPMPENGQTEENDWILMGSTOEAKKNANMKNRRIGSGSG 617
OY 61 FFDEENGKNGALNLFNGKSAQNRFLLTGANLNGKISVTGG 104
DB 618 FFGEENGKNGALNLFNGKSAQNRFLLTGTLNKGISVTGG 661

RESULT 10
O51169 PRELIMINARY; PRT; 1561 AA.
AC O51169;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE IGAI PROTEASE.
GN IGA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN-HR13;
RA MEDLINE-95302961; PubMed=7783620;
RA Lomholt H., Poulsen K., Mogens K.;
RT "Comparative characterization of the iga gene encoding IgA1 protease
RT in Neisseria meningitidis, Neisseria gonorrhoeae and Haemophilus
RT influenzae."
RL Mol. Microbiol. 15:495-506(1995).
DR EMBL; X82474; CA57857.1; -
DR MEROPS; S06.001; -
DR INTERPRO; IPR000710; -
DR INTERPRO; IPR002195; -
DR PRINTS; PR00921; IGASERPTASE.
DR PROSITE; PS00482; DIHYDROOROTASE_1; UNKNOWN_1.
KM Protease.
SQ SEQUENCE 1561 AA; 171848 MW; 1C96E291A00017D5 CRC64;

Query Match 87.4%; Score 494; DB 2; Length 1561;
Best Local Similarity 87.5%; Pred. No. 1.7e-43;
Matches 91; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
OY 1 LYKRYRYALKSGRLNAPMPENGVAENNDWIFMGYTOEARKNANMKNRRIGDFGG 60
DB 584 LYKRYRYALKSGSVNAPMPENGQTEENDWILMGSTOEAKKNANMKNRRIGSGSG 643
OY 61 FFDEENGKNGALNLFNGKSAQNRFLLTGANLNGKISVTGG 104
DB 644 FFGEENGKNGALNLFNGKSAQNRFLLTGTLNKGISVTGG 687

RESULT 11
O9JVB9 PRELIMINARY; PRT; 1773 AA.
AC O9JVB9;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE IGAI PROTEASE (EC 3.4.21.7).
GN IGA OR NMA0905.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN-22491 / SEROTYPE 4A;
RA MEDLINE-20222556; PubMed-10761919;
RA Parkhill J., Achtmann M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davids R.M., Davis P., Devlin K., Feltham T., Hamlin N., Holroyd S.,
RA Jagers K., Leach S., Mouton S., Mungall K., Quail M.A.,
RA Rajandream K.A., Rutherford K.M., Stammers M., Stelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;

Tue May 1 15:15:53 2001

us-09-142-970-5.ra1

Page 1

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 1, 2001, 14:59:31 ; Search time 37.5 Seconds

(without alignments)
53.278 Million cell updates/sec

Title: US-09-142-970-5

Sequence: 1 LYXKNRYRYALKSGRLNAP.....NRLTLTGANLNKISVTG 104

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Sequences: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	ID	Description
2	556	98.4	1507	6	5268270-2
3	298.5	52.8	1541	6	PCT-US95-10661A-3
4	291.5	51.6	1545	5	PCT-US95-10661A-4
5	291.5	51.6	1702	5	PCT-US95-10661A-5
6	281.5	49.8	1848	5	PCT-US95-10661A-6
7	101	17.9	1394	5	PCT-US95-10661A-2
8	72.5	12.8	605	1	US-08-462-884A-3
9	72.5	12.8	605	1	US-08-461-881B-3
10	70	12.4	1577	2	US-08-123-960-3
11	67.5	11.9	631	1	US-08-793-824-2
12	67.5	11.9	631	1	US-08-487-890A-111
13	67.5	11.9	631	2	US-08-478-435-111
14	67.5	11.9	631	2	US-08-337-483-111
15	67.5	11.9	631	2	US-08-478-373-111
16	67.5	11.9	631	3	US-08-474-671-111
17	66.5	11.8	631	3	US-08-483-577A-111
18	66.5	11.8	631	1	US-08-487-890A-115
19	66.5	11.8	631	2	US-08-478-435-115
20	66.5	11.8	631	2	US-08-337-483-115
21	66.5	11.8	631	3	US-08-478-373-115
22	66.5	11.8	631	3	US-08-474-671-115
23	66	11.7	1536	1	US-08-483-577A-115
24	66	11.7	1536	1	US-08-038-682-2
25	66	11.7	1536	2	US-08-302-832-2
26	66	11.7	1536	2	US-08-530-198-2
27	66	11.7	1536	2	US-08-469-880-2
					US-08-728-470-2

28	66	11.7	1536	2	US-08-617-697-2	Sequence 2, Appl1
29	64.5	11.4	644	1	US-08-487-890A-6	Sequence 6, Appl1
30	64.5	11.4	644	2	US-08-478-435-6	Sequence 6, Appl1
31	64.5	11.4	644	2	US-08-337-483-6	Sequence 6, Appl1
32	64.5	11.4	644	2	US-08-478-373-6	Sequence 6, Appl1
33	64.5	11.4	644	3	US-08-474-671-6	Sequence 6, Appl1
34	64.5	11.4	644	3	US-08-483-577A-6	Sequence 6, Appl1
35	64.5	11.4	671	2	US-08-737-716-13	Sequence 13, Appl1
36	63.5	11.2	421	2	US-08-807-263-4	Sequence 13, Appl1
37	63.5	11.2	532	4	US-08-899-324-33	Sequence 33, Appl1
38	63.5	11.2	532	2	US-08-329-892B-33	Sequence 33, Appl1
39	63.5	11.2	597	1	US-08-462-884A-1	Sequence 1, Appl1
40	63.5	11.2	597	1	US-08-461-881B-1	Sequence 1, Appl1
41	63.5	11.2	597	2	US-09-123-960-1	Sequence 1, Appl1
42	63.5	11.2	759	2	US-08-450-351-2	Sequence 2, Appl1
43	63.5	11.2	759	2	US-08-450-351-2	Sequence 2, Appl1
44	63	11.2	1290	1	US-08-138-641-2	Sequence 2, Appl1
45	63	11.2	1290	1	US-08-138-133-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
5268270-2
Patent No. 5268270
APPLICANT: Bayer, Thomas F. Halter, Roman, Pohlner, Johannes
TITLE OF INVENTION: PROCESS FOR PRODUCING PROTEINS USING GRAM
NEGATIVE HOST CELLS
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/171,872
FILING DATE: 01-JUL-1987
SEQ ID NO: 2
LENGTH: 1507
5268270-2

Query Match 98.4%; Score 556; DB 6; Length 1507;
Best Local Similarity 99.0%; Pred. No. 1e-58;
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LYXKNRYRYALKSGRLNAPMPENGVAENNDMPKQTOEARKNMMKNNRRIGDGG 60
DB 559 LYXKNRYRYALKSGRLNAPMPENGVAENNDMPKQTOEARKNMMKNNRRIGDGG 618
QY 61 FEDEENGKGNALNINFNKSNQNRFLTLTGANLNKISVTG 104
DB 619 FEDEENGKGNALNINFNKSNQNRFLTLTGANLNKISVTG 662

RESULT 2
PCT-US95-10661A-3
Sequence 3, Application PC/TUS9510661A
GENERAL INFORMATION:
APPLICANT: Washington University, et al.
TITLE OF INVENTION: Haemophilus Adherence and Penetration Protein
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patently Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10661A
FILING DATE: 01-JUL-1987

Tue May 1 15:15:31 2001

us-09-142-970-1.1rag

Page 4

Seq. 1

RESULT 6
W61605 standard; peptide; 104 AA.
W61605:
27-OCT-1998 (first entry)
Neisseria IgA1 protease fragment 4.
Immunoglobulin protease; carrier: paediatric; vaccine:
epidemic bacterial infection; Neisseria; Haemophilus; T-cell.
Neisseria sp.
W09831791-A1.
23-JUL-1998.
20-JAN-1998; 98WO-EP00294.
21-JAN-1997; 97EP-0100883.
(PLAC) MAX PLANCK GES FOENDERUNG WISSENSCHAFTEN.
(INNER) PASTEUR MERIEUX SERUMS & VACCINS SA.
Achtmann M, Moreau M;
WPI: 1998-414092/35.
New peptide from Neisseria immunoglobulin protease - useful as
immunogenic carrier, e.g. particularly for polysaccharide(s),
forming conjugates used in vaccines against Neisseria and
Haemophilus
Claim 2; Fig 1/4; 32pp; English.
The Neisseria immunoglobulin protease fragments W61602-W61606 are used
as carriers for a conjugate, particularly in combination with a
polysaccharide. They can be used in paediatric or other vaccines,
particularly for prevention of epidemic bacterial infections, especially
those caused by Neisseria or Haemophilus. The protease fragment is a
highly immunogenic carrier that elicits a T-cell response, resulting in a
long-lasting memory and high antibody titre, and possibly making possible
vaccination without adjuvant.

Query Match 81.2%; Score 453; DB 19; Length 104;
Best Local Similarity 84.5%; Pred. No. 2.3e-45;
Matches 82; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
OY 1 LYYKNRYRYALKSGSVNAPMPENGOTENNNDWLMGSTOEAKKNAHKNRISGFSG 60
DB 1 LYYKNRYRYALKSGSVNAPMPENGOTENNNDWLMGSTOEAKKNAHKNRISGFSG 60
OY 61 FFEENGKGHNGALNLFNGSKSAQNRFLTGSTNLNGKISYVTOG 97
DB 61 fideengkgngalnlnfngksaqrfltlgtnganlg 97
RESULT 7
R07304 standard; protein; 1541 AA.
R07304:
31-JAN-1991 (first entry)
IgA1 protease.

XX XX
KW IgA1; vaccine; meningitis; gonorrhoea; allergies.
XX OS Haemophilus influenzae.
XX PN W09011367-A.
XX PD 04-OCT-1990.
XX PF 16-MAR-1990; 90WO-DK00073.
XX PR 17-MAR-1989; 89DK-0001308.
XX PA (KILI/) KILIAN M.
XX PI Kilian M, Poulsen K;
XX DR WPI: 1990-320267/42.
XX DR N-PSDB; 006164.
XX PT Immunoglobulin A1 protease prodn. - by cloning from
PT microorganisms for immunisation against immunoglobulin A1
PT protease producing bacteria
PS Disclosure; fig 3; 44pp; English.
XX CC This immunoglobulin (Ig)A1 protease is produced by recombinant DNA
XX CC methods. It is useful in a vaccine for e.g. meningococcal meningitis,
XX CC gonorrhoea or allergic diseases. It specifically cleaves the heavy
XX CC chain of human IgA1 in the hinge region.
SQ Sequence 1541 AA;

Query Match 59.1%; Score 329.5; DB 11; Length 1541;
Best Local Similarity 56.7%; Pred. No. 2e-29;
Matches 59; Conservative 19; Mismatches 25; Indels 1; Gaps 1;
OY 1 LYYKNRYRYALKSGSVNAPMPENGOTENNNDWLMGSTOEAKKNAHKNRISGFSG 60
DB 595 lnylytyalkrgastsejpksgsenewlymgtksdeakrnmhinnermgfng 654
OY 61 FFEENGKGHNGALNLFNGSKSAQNRFLTGSTNLNGKISYVTOG 104
DB 655 yfgeegk-ngnlnvtlkygseqnrflltgsnlnlgdlvtekg 697
RESULT 8
Y38825
ID Y38825 standard; protein; 1468 AA.
Y38825:
08-OCT-1999 (first entry)
DE Neisseria gonorrhoeae antigenic protein encoded by ORF1.
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW treatment; Neisseria infection; meningitis; septicaemia; gonorrhea.
XX OS Neisseria gonorrhoeae.
XX PN W09924578-A2.
XX PD 20-MAY-1999.
XX PF 09-OCT-1998; 98WO-IB01665.
XX PR 01-SEP-1998; 98GB-0019016.
XX PR 06-NOV-1997; 97GB-0023516.
XX PR 14-NOV-1997; 97GB-0024190.
XX PR 18-NOV-1997; 97GB-0024386.
XX PR 27-NOV-1997; 97GB-0025158.

|||||

|||||

|||||

Seq 10.10.2

RESULT 6
ID W61605 standard; peptide; 104 AA.
AC W61605;
DT 27-OCT-1998 (first entry)
DE Neisseria IgA1 protease fragment 4.
KM Immunoglobulin protease; carrier; paediatric; vaccine;
KW epidemic bacterial infection; Neisseria; Haemophilus; T-cell.
XX
OS Neisseria sp.
PI W61605-1751-A1.
XX
PD 23-JUL-1998.
XX
PF 20-JAN-1998; 98WO-EP00294.
XX
PR 21-JAN-1997; 97EP-0100883.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX (INMR) PASTEUR MERIEUX SERUMS & VACCINS SA.
XX
PI Achtmann M, Moreau M;
XX
DR WPI; 1998-414092/35.
XX
PT New peptide from Neisseria immunoglobulin protease - useful as
PT immunogenic carrier, e.g. particularly for polysaccharide(s),
PT forming conjugates used in vaccines against Neisseria and
PT Haemophilus
XX
PS Claim 2; Fig 1/4; 32pp; English.
XX
CC The Neisseria immunoglobulin protease fragments W61602-W61606 are used
CC as carriers for a conjugate, particularly in combination with a
CC polysaccharide. They can be used in paediatric or other vaccines,
CC particularly for prevention of epidemic bacterial infections, especially
CC those caused by Neisseria or Haemophilus. The protease fragment is a
CC highly immunogenic carrier that elicits a T-cell response, resulting in a
CC long-lasting memory and high antibody titre, and possibly making possible
CC vaccination without adjuvant.
XX
SO Sequence 104 AA.

Query Match 84.5%; Score 475; DB 19; Length 104;
Best Local Similarity 88.7%; Pred. No. 1.7e-47;
Matches 86; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 LYKKNRYIAKSGSVNAPMPENGVTENNDFMGVTOEAKKMANHKNORISGFSG 60
DB 1 LYKKNRYIAKSGSVNAPMPENGVTENNDFMGVTOEAKKMANHKNORISGFSG 60
OY 61 PFGEENGKGNALNLFNGKSAQNRFLLTGGTNLNG 97
DB 61 fideengkgnalnlnfngksaqnrflltgganlng 97

RESULT 7
ID R07304 standard; protein; 1541 AA.
XX
XX R07304;
XX
XX AN-1991 (first entry)

XX
KM IgA1; vaccine; meningitis; gonorrhoea; allergy.
XX
OS Haemophilus influenzae.
XX
PN W09011367-A.
XX
PD 04-OCT-1990.
XX
PF 16-MAR-1990; 90WO-DK00073.
XX
PR 17-MAR-1989; 89DK-0001308.
XX
PA (KILIAN) KILIAN M.
XX
PI Kilian M, Poulsen K;
XX
DR WPI; 1990-32036/42.
XX
PT microorganisms for immunisation against immunoglobulin A1
PT protease producing bacteria
XX
PS Disclosure; fig 3; 44pp; English.
XX
CC This immunoglobulin (Ig)A1 protease is produced by recombinant DNA
CC methods. It is useful in a vaccine for e.g. meningococcal meningitis,
CC gonorrhoea or allergic diseases. It specifically cleaves the heavy
CC chain of human IgA1 in the hinge region.
XX
SO Sequence 1541 AA;

Query Match 58.6%; Score 329.5; DB 11; Length 1541;
Best Local Similarity 56.7%; Pred. No. 3.9e-29;
Matches 59; Conservative 20; Mismatches 24; Indels 1; Gaps 1;

OY 1 LYKKNRYIAKSGSVNAPMPENGVTENNDFMGVTOEAKKMANHKNORISGFSG 60
DB 595 lnlennyialrkqastseipkngesenwlymgtlsdeakrnmhlnnermgfng 654
OY 61 PFGEENGKGNALNLFNGKSAQNRFLLTGGTNLNGISVTG 104
DB 655 yfgeegk-nmgnlnvctkqsegrflltggtnlndltvekg 697

RESULT 8
ID Y75564 standard; protein; 1431 AA.
XX
AC Y75564;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria meningitidis ORF 759 protein sequence SEQ ID NO:2602.
XX
KM Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy.
XX
OS Neisseria meningitidis.
XX
PN W09957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US09346.
XX
PR 01-MAY-1998; 98US-0083758.
PR 31-JUL-1998; 98US-0094869.
PR 02-SEP-1998; 98US-0098994.
PR 02-SEP-1998; 98US-0099062.

us-09-142-970-3.rag

528 1020:3

528 100A

XX IgA1; vaccine; meningitis; gonorrhoea; allergies.
XX
XX Haemophilus influenzae.
OS MO9011367-A.
PN
XX 04-OCT-1990.
PD
XX
XX 16-MAR-1990; 90MO-DK00073.
PF
XX 17-MAR-1989; 89DK-0001308.
PR
XX
XX (KILI/) KILIAN M.
PA
XX
XX Killan M, Poulsen K;
PI
XX WPI; 1990-320267/42.
XX DR
XX N-PSDB; Q06164.
DR
XX
XX Immunoglobulin A1 protease prodn. - by cloning from
PT microorganisms for immunisation against immunoglobulin A1
PT protease producing bacteria
XX
XX
XX Disclosure: fig 3; 44pp: English.
XX
XX
XX This immunoglobulin (IgA)1 protease is produced by recombinant DNA
CC methods. It is useful in a vaccine for e.g. meningococcal meningitis
CC gonorrhoea or allergic diseases. It specifically cleaves the heavy
CC chain of human IgA1 in the hinge region.
XX
XX
XX Sequence 1541 AA;
50

Query Match	56.9%	Score 320.5	DB 11	Length 1541
Best Local Similarity	54.8%	Pred. No. 1	Le-27	
Matches 57	Conservative	21	Mismatches 25	Indels 1
				Gaps
OY	1	LYKNRYRYALKSGGVNAPMPENGGCFENNNDWVFMGYKOEAEQAKNNANHHKNNORISGFSG	60	
Db	595	lnlenlytalyatkgsatrseelpkngsgesnenwlymgtksdeakrnmhlnnermgfng	654	
OY	61	PFGEENGKHGNCALNLNFGKSAQNRFLTGSTNLNGKISVTCG	104	
Db	655	yfgeegk-ngnlnhvtfkgsqgnrflttgtnlngtlvtekg	697	
RESULT	8			
ID	Y75564	Y75564 standard; Protein: 1431 AA.		
XX	Y75564;			
XX	21-MAR-2000	(first entry)		
DE	Neisseria meningitidis ORF 759	protein sequence SEQ ID NO:2602.		
XX	Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;			
KW	antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;			
KW	antibacterial; gene therapy.			
XX	Neisseria meningitidis.			
OS	Neisseria meningitidis.			
XX	MO9957280-A2.			
PN	11-NOV-1999.			
XX	30-APR-1999;	99MO-USO9346.		
PD	98US-0083758.			
XX	31-JUL-1998;	98US-0094869.		
PR	02-SEP-1998;	98US-0098994.		
PR	02-SEP-1998;	98US-0099062.		

Se 8 10NOV4

RESULT 6
ID W61602 standard: peptide: 105 AA.
XX W61602:
AC 27-OCT-1998 (first entry)
XX
DE Neisseria IgA1 protease fragment 1.
XX
KM Immunoglobulin protease; carrier: paediatric; vaccine;
epidemic bacterial infection; Neisseria; Haemophilus; T-cell.
XX
OS Neisseria sp.
XX
PI MO9831791-A1.
XX
PD 23-JUL-1998.
XX
PF 20-JAN-1998; 98WO-EP00294.
XX
PR 21-JAN-1997; 97EP-0100883.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI (INMR) PASTEUR MERIEUX SERUMS & VACCINS SA.
XX
PI Achtmann M, Moreau M;
XX
DR WPI: 1998-414092/35.
XX
PT New peptide from Neisseria immunoglobulin protease - useful as
immunogenic carrier, e.g. particularly for polysaccharide(s),
PT forming conjugates used in vaccines against Neisseria and
PT Haemophilus
XX
PS Claim 6; Page 10; 32pp; English.
XX
CC The Neisseria immunoglobulin protease fragments W61602-W61606 are used
as carriers for a conjugate, particularly in combination with a
CC polysaccharide. They can be used in paediatric or other vaccines,
CC particularly for prevention of epidemic bacterial infections, especially
CC those caused by Neisseria or Haemophilus. The protease fragment is a
CC highly immunogenic carrier that elicits a T-cell response, resulting in a
CC long-lasting memory and high antibody titre, and possibly making possible
CC vaccination without adjuvant.
XX
SQ Sequence 105 AA:

Query Match 79.6%; Score 453; DB 19; Length 105;
Best Local Similarity 84.5%; Pred. No. 1.7e-44;
Matches 82; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
OY 1 LYYKNRYRYALKSGRLNAMPENGVAENNDWFMGYTOEARKNMMNNKRRIGDFG 60
DB 2 LYYKNRYRYALKSGSVNAPENGQTENDWLMSTGEAKKNMHNKNGRISGFSG 61
OY 61 FDEENGKGNHGNALNPNNGSKSAONRFLTGANLNG 97
DB 62 ffgengkgngalnlnlntngksqnrfllygtcngln 98

RESULT 7
ID R07304 standard: protein: 1541 AA.
XX R07304:
XX N-1991 (first entry)

XX
XX IgA1; vaccine; meningitis; gonorrhoea; allergies.
XX
XX Haemophilus influenzae.
XX
XX WO9011367-A.
XX
XX 04-OCT-1990.
XX
XX 16-MAR-1990; 90WO-DK00073.
XX
XX 17-MAR-1989; 89DK-0001308.
XX
XX (KIL/) KILIAN M.
XX
XX Killian M, Poulsen K;
XX
XX WPI: 1990-320267/42.
XX
XX N-PSDB; Q06164.
XX
XX Immunoglobulin A1 protease prodn. - by cloning from
PT microorganisms for immunisation against immunoglobulin A1
PT protease producing bacteria
XX
XX Disclosure; fig 3; 44pp; English.
XX
XX This immunoglobulin (IgA1) protease is produced by recombinant DNA
XX methods. It is useful in a vaccine for e.g. meningococcal meningitis,
XX gonorrhoea or allergic diseases. It specifically cleaves the heavy
XX chain of human IgA1 in the hinge region.
XX
SQ Sequence 1541 AA:

Query Match 49.5%; Score 281.5; DB 11; Length 1541;
Best Local Similarity 48.2%; Pred. No. 2.1e-23;
Matches 54; Conservative 17; Mismatches 30; Indels 11; Gaps 2;
OY 1 LYYKNRYRYALKSGRLNAMPENGVAENNDWFMGYTOEARKNMMNNKRRIGDFG 60
DB 595 lntenylyalrtyaastrelprkngesenwlymgtksdeakrvnmhlnrmermgfng 654
OY 61 FDEENGKGNHGNALNPNNGSKSAONRFLTGANLNG-----NGRP 102
DB 655 yfgeegk-nngalnvtfkxseqnrllygtcnglnlgdlevkgtlflsgpr 705
RESULT 8
ID Y75564 standard: protein: 1431 AA.
XX
XX Y75564:
XX
XX 21-MAR-2000 (first entry)
XX
XX Neisseria meningitidis ORF 759 protein sequence SEQ ID NO:2602.
XX
XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
XX antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
XX antibacterial; gene therapy.
XX
XX Neisseria meningitidis.
XX
XX WO9957280-A2.
XX
XX 11-NOV-1999.
XX
XX 30-APR-1999; 99WO-US09346.
XX
XX 01-MAY-1996; 98US-0083758.
XX
XX 31-JUL-1998; 98US-0094869.
XX
XX 02-SEP-1998; 98US-0098994.
XX
XX 02-SEP-1998; 98US-0099062.

